



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 142220

To: Nita M Minnifield
Location: rem/3c01/3c18
Art Unit: 1645
Monday, January 24, 2005

Case Serial Number: 09/837344

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

*Reviewed
2-1-05
mm.*

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 22, 2005, 20:53:48 ; Search time 4375 Seconds
(without alignments)
16019.048 Million cell updates/sec

Title: US-09-837-344-41

Perfect score: 1482

Sequence: 1 CAAGAACAAACAAAGCGATCT.....AATATTTTATGAAACTATAA 1482

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1482	100.0	1482	6	AR162970 Sequence
2	1482	100.0	1482	6	AR178259 Sequence
3	1482	100.0	1482	3	PF162974 Sequence
4	1480.4	99.9	1482	6	AR162974 Sequence
5	1480.4	99.9	1482	6	AR178263 Sequence
6	1446	97.6	1493	6	A28743 CDNA for LS
7	1446	97.6	1493	6	AR162967 Sequence
8	1446	97.6	1493	6	AR178256 Sequence
9	1442	97.3	5970	3	PF162974 Sequence
10	1406.8	94.9	253001	3	AB014834 Plasmid
11	950	64.1	950	6	A28740 CDNA for LS
12	950	64.1	950	6	AR162961 Sequence
13	950	64.1	950	6	AR178250 Sequence
14	843	56.9	843	3	PF162974 Sequence
15	841.4	56.8	843	3	PF162974 Sequence
16	841.4	56.8	843	3	PF162974 Sequence
17	841.4	56.8	843	3	PF162974 Sequence
18	841.4	56.8	843	3	PF162974 Sequence
19	839.8	56.7	843	3	PF162974 Sequence

20	839.8	56.7	843	3	PF162974 Sequence
21	839.8	56.7	843	3	PF162974 Sequence
22	839.8	56.7	843	3	PF162974 Sequence
23	838.2	56.6	843	3	PF162974 Sequence
24	836.6	56.5	843	3	PF162974 Sequence
25	836.6	56.5	843	3	PF162974 Sequence
26	836.6	56.5	843	3	PF162974 Sequence
27	836.6	56.5	843	3	PF162974 Sequence
28	835	56.3	843	3	PF162974 Sequence
29	835	56.3	843	3	PF162974 Sequence
30	833.4	56.2	843	3	PF162974 Sequence
31	833.4	56.2	843	3	PF162974 Sequence
32	791.8	53.4	795	3	AF246996 Plasmid
33	472.8	31.9	988	6	A28742 CDNA for LS
34	472.8	31.9	988	6	AR162963 Sequence
35	472.8	31.9	988	6	AR178252 Sequence
36	472.8	31.9	988	6	AR162966 Sequence
37	470.8	31.8	954	6	AR178255 Sequence
38	470.8	31.8	954	6	AR178255 Sequence
39	274.4	18.5	208332	10	AC122227 Mus muscu
40	252.4	17.0	172716	2	AC115383 Rattus no
41	250.8	16.9	184015	10	AC144849 Mus muscu
42	242.6	16.4	208485	2	AC149597 Mus muscu
43	225.8	15.2	2069	6	E10125 DNA encodin
44	225.8	15.2	3389	6	E10126 DNA encodin
45	215.8	14.6	110000	2	AC129389_1 Continuation (2 of

ALIGNMENTS

RESULT 1	AR162970	1482 bp	DNA	linear	PAT 17-OCT-2001
LOCUS	AR162970	Sequence 41 from patent US 6270771.			
DEFINITION	AR162970				
ACCESSION	AR162970				
VERSION	AR162970.1	GI:16233435			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1482)				
AUTHORS	Guertin-Marchand, C. and Druilhe, P.				
TITLE	Peptide sequences specific for the hepatic stages of P. falciparum bearing epitopes capable of stimulating the T lymphocytes				
JOURNAL	Patent: US 6270771-A 41 07-AUG-2001;				
FEATURES	Location/Qualifiers				
source	1..1482				
ORIGIN	/organism="unknown"				
	/mol_type="unassigned DNA"				

Query Match	100.0%	Score 1482;	DB 6;	Length 1482;
Best Local Similarity	100.0%	Pred. No. 6,9e-179;		
Matches 1482;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CAAGAACAAACAAAGCGATCTAGAACAGAGACGCTTAAGAAAGTTGCAAGACAA	60	
DB	1	CAAGAACAAACAAAGCGATCTAGAACAGAGACGCTTAAGAAAGTTGCAAGACAA	60	
QY	61	CAAGGATTTAGAAAGATAGACTTCTTAAGAAAGTTGCAAGAGCAAGACGAT	120	
DB	61	CAAGGATTTAGAAAGATAGACTTCTTAAGAAAGTTGCAAGAGCAAGACGAT	120	
QY	121	TTAGAACAGAGAGACTTCTTAAGAAAGTTGCAAGACAAAGGATCTAGAACAA	180	
DB	121	TTAGAACAGAGAGACTTCTTAAGAAAGTTGCAAGACAAAGGATCTAGAACAA	180	
QY	181	GAGAGCGTGTCTTAAGAAAGTTGCAAGACAAAGGATTTAGAACAGAGACGCT	240	
DB	181	GAGAGCGTGTCTTAAGAAAGTTGCAAGACAAAGGATTTAGAACAGAGACGCT	240	
QY	241	GCTAAAGAAAGTGTGCAAGACAAAGCGATTTAGAACAGTGAAGTCTTAAGAA	300	

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OM nucleic - nucleic search, using sw model

Run on: January 22, 2005, 20:50:38 ; Search time 533 Seconds

(without alignments)
14595.951 Million cell updates/sec

Title: US-09-837-344-41

Sequence: 1482
1 CAGACACACAAAGCATCT.....AATATTATGAACTATA 1482

Scoring table: IDENTITY_NUC

Searched: 4134886 segs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: geneseqn2000s:*
5: geneseqn2001as:*
6: geneseqn2001bs:*
7: geneseqn2002as:*
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9: geneseqn2003as:*
10: geneseqn2003bs:*
11: geneseqn2003as:*
12: geneseqn2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1482	100.0	1496	2	AAQ28119	AaQ28119 P.falcipa
2	950	64.1	950	2	AAQ28115	AaQ28115 P.falcipa
3	853.2	57.6	1320	2	AAQ80916	AaQ80916 Plasmodiu
4	586.4	39.6	1566	2	AAQ05140	AaQ05140 Sequence
5	503.4	34.0	1371	12	ADO21941	AdO21941 LSA-NRCH
6	493.6	33.3	1374	12	ADO21919	AdO21919 LSA-NRCH
7	472.8	31.9	988	2	AAQ28117	AaQ28117 P.falcipa
8	233.4	15.7	1300	12	ADP85917	AdP85917 Synthetic
9	225.8	15.2	3399	2	AAT05868	AaT05868 Chicken 1
10	183.2	12.4	210	1	AAN80899	AaA80899 Sequence
11	179.4	12.1	1686	3	AAQ70099	AaQ70099 Plasmodiu
12	176.6	11.9	3579	3	AAQ70099	AaQ70099 Plasmodiu
13	170.6	11.5	1998	3	AAA70212	AaA70212 Plasmodiu
14	151.2	10.2	6292	4	AAQ46735	AaQ46735 Tumour su
15	149.2	10.1	6767	4	AAQ46735	AaQ46735 Tumour su
16	146	9.9	3662	4	AAQ46735	AaQ46735 Tumour su
17	139.4	9.4	9539	6	ABK28180	AbK28180 DNA trans
18	139.4	9.3	6668	6	ABU33697	AbU33697 Human imm
19	137.8	9.2	6644	6	AAQ33181	AaQ33181 Base sequ
20	136.4	9.2	7372	2	AAQ33182	AaQ33182 Base sequ
21	136.4	9.2	7372	2	AAQ33182	AaQ33182 Base sequ

22	136.4	9.2	7797	2	AAQ33180	AaQ33180 Cowpox vi
23	136.4	9.2	7996	2	AAQ33184	AaQ33184 Base sequ
24	132.8	9.0	778	2	ABQ15588	AbQ15588 Oligonuc
25	132.8	9.0	778	2	ABQ15588	AbQ15588 Oligonuc
26	131.4	8.9	7442	4	AAQ46686	AaQ46686 Tumour su
27	129.8	8.8	1762	6	ABQ20939	AbQ20939 Oligonuc
28	129.8	8.8	1762	6	ABQ20939	AbQ20939 Oligonuc
29	129.2	8.7	1995	6	ABQ20942	AbQ20942 Oligonuc
30	129.2	8.7	1995	6	ABQ20943	AbQ20943 Oligonuc
31	129	8.7	1200	6	ABQ39210	AbQ39210 Oligonuc
32	129	8.7	1200	6	ABQ39211	AbQ39211 Oligonuc
33	129	8.7	7597	6	ABQ33013	AbQ33013 Human imm
34	129	8.7	14006	6	ABQ33958	AbQ33958 Human imm
35	127.4	8.6	3683	8	ABQ10199	AbQ10199 Haematopo
36	127.4	8.6	3683	8	ABQ10199	AbQ10199 Haematopo
37	123.4	8.3	3037	6	ABQ54066	AbQ54066 Oligonuc
38	123.4	8.3	3037	6	ABQ54067	AbQ54067 Oligonuc
39	123	8.3	12237	6	ABQ34358	AbQ34358 Human imm
40	120.4	8.1	1533	8	ACQ28672	AcQ28672 Prokaryot
41	120.4	8.1	6419	6	ABQ32267	AbQ32267 Human imm
42	118.6	8.0	975	6	ABQ29508	AbQ29508 Oligonuc
43	118.6	8.0	975	6	ABQ29509	AbQ29509 Oligonuc
44	118.6	8.0	7758	6	ABQ33103	AbQ33103 Human imm
45	117.8	7.9	6898	6	ABQ80222	AbQ80222 Human che

ALIGNMENTS

RESULT 1	AAQ28119	standard; DNA; 1496 BP.
ID	AAQ28119	
AC	AAQ28119;	
XX		
DT	25-MAR-2003	(revised)
XX		
DT	08-FEB-1993	(first entry)
XX		
DE	P.falciparum LSA gene 3' region.	
XX		
KM	Malaria; hepatocyte; sporozoite; T-cell epitope; B-cell epitope;	
KM	paludism; liver stage-specific antigen; ss.	
XX		
OS	Plasmodium falciparum.	
XX		
XX		
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FT	CDS	1..1482
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FT		/product= "LSA_C-terminal_region"
FT	repeat_region	37..639
FT		/*tag= a
FT	repeat_unit	37..87
FT		/*tag= b
FT		/rpt_type= TANDEM
XX		
PD	WO9213884-A1.	
XX		
PD	20-AUG-1992.	
XX		
PF	05-FEB-1992;	92WO-FR000104.
XX		
PR	05-FEB-1991;	91FR-00001286.
XX		
PA	(INSP) INST PASTEUR.	
XX		
PI	Guerinmarchand C, Druilhe P;	
XX		
DR	WPI. 1992-299885/36.	
XX		
DR	P-PSDB; AAK26944.	
XX		
PT	Polypeptide(s) derived from liver stage of PLASMODIUM FALCIPARUM - for	
PT	vaccination against, treatment of and diagnosis of malaria.	
XX		

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OM nucleic - nucleic search, using sw model

Run on: January 22, 2005, 23:08:59 ; Search time 101 Seconds
(without alignments)
10429.595 Million cell updates/sec

Title: US-09-837-344-41

Perfect score: 1482
Sequence: 1 CAAGAACCAACAAAGCATCT.....AAATTTTATGAACCTATA 1482

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/prodata/1/ina/5A.COMB.seq.*
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3: /cgn2_6/prodata/1/ina/5A.COMB.seq.*
4: /cgn2_6/prodata/1/ina/5B.COMB.seq.*
5: /cgn2_6/prodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1482	100.0	1482	3	US-08-098-327E-41 Sequence 41, Appl
2	1482	100.0	1482	3	US-08-462-625-41 Sequence 41, Appl
3	1480.4	99.9	1482	3	US-08-098-327E-45 Sequence 45, Appl
4	1480.4	99.9	1482	3	US-08-462-625-45 Sequence 45, Appl
5	1446	97.6	1493	3	US-08-098-327E-38 Sequence 38, Appl
6	1446	97.6	1493	3	US-08-462-625-38 Sequence 38, Appl
7	950	64.1	950	3	US-08-098-327E-32 Sequence 32, Appl
8	950	64.1	950	3	US-08-462-625-32 Sequence 32, Appl
9	853.2	57.6	1320	1	US-08-257-073-15 Sequence 15, Appl
10	472.8	31.9	988	3	US-08-098-327E-34 Sequence 34, Appl
11	472.8	31.9	988	3	US-08-462-625-34 Sequence 34, Appl
12	470.8	31.8	954	3	US-08-098-327E-37 Sequence 37, Appl
13	470.8	31.8	954	3	US-08-462-625-37 Sequence 37, Appl
14	116.2	7.8	3095	6	5231168-1 Patent No. 5231168
15	1837	7.5	1837	4	US-09-270-767-1308 Sequence 1308, Ap
16	111.6	7.5	1837	4	US-09-270-767-16550 Sequence 16590, A
17	110.2	7.4	7218	1	US-08-232-463-14 Sequence 14, Appl
18	101.2	6.8	1956	3	US-08-559-8968-1 Sequence 1, Appl
19	101.2	6.8	1956	3	US-09-351-794A-1 Sequence 1, Appl
20	93.6	6.3	5361	3	US-08-973-462-2 Sequence 2, Appl
21	93.6	6.3	5361	3	US-08-973-462-2 Sequence 2, Appl
22	89.6	6.0	1664976	4	US-08-916-421B-1 Sequence 1, Appl
23	89.6	6.0	1664976	4	US-08-692-570-1 Sequence 1, Appl
24	88.4	6.0	5340	4	US-09-627-122-21 Sequence 21, Appl
25	86.8	5.9	699	4	US-09-248-796A-9722 Sequence 9722, Ap
26	86.8	5.9	4766	5	PCT-US93-07261-10 Sequence 10, Appl
27	83.2	5.6	1669	3	US-09-461-697-184 Sequence 184, App

28	82.8	5.6	19124	2	US-08-487-826B-13 Sequence 13, Appl
29	81.6	5.5	5455	4	US-10-204-708-33 Sequence 33, Appl
30	81.4	5.5	2223	1	US-08-257-073-4 Sequence 4, Appl
31	81.2	5.5	696	3	US-09-461-697-193 Sequence 193, App
32	81.2	5.5	699	3	US-09-461-697-191 Sequence 191, App
33	81.2	5.5	717	3	US-09-461-697-189 Sequence 189, App
34	81.2	5.5	774	3	US-09-461-697-187 Sequence 187, App
35	81.2	5.5	819	3	US-09-461-697-185 Sequence 185, App
36	80.2	5.4	6669	4	US-10-204-708-6 Sequence 6, Appl
37	79.6	5.4	53332	4	US-09-801-861-3 Sequence 3, Appl
38	79.6	5.4	53332	4	US-10-224-562-3 Sequence 3, Appl
39	78.4	5.3	8961	4	US-10-204-708-80 Sequence 80, Appl
40	78.2	5.3	10640	4	US-09-417-485D-5 Sequence 5, Appl
41	76.8	5.2	396	4	US-09-640-173-53 Sequence 53, Appl
42	76.8	5.2	396	4	US-09-713-550-53 Sequence 53, Appl
43	76.8	5.2	396	4	US-09-825-294-53 Sequence 53, Appl
44	76.8	5.2	396	4	US-09-970-966-53 Sequence 53, Appl
45	76.8	5.2	705	4	US-09-270-767-5061 Sequence 5061, Ap

ALIGNMENTS

RESULT 1
US-08-098-327E-41
Sequence 41, Application US/08098327E
Patent No. 6270771
GENERAL INFORMATION:
APPLICANT: GUERIN-MARCHAND, Claudine
APPLICANT: DRUILHE, Pierre
TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE
TITLE OF INVENTION: HEPATIC STAGES OF P. FALCIPARUM BEARING EPTOTPS CAPABLE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSER: Burns, Doane, Swecker & Machis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/098,327E
FILING DATE: 24-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 01286
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 010830-045
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 1482 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1482
PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO 92/13884
PUBLICATION DATE: 20-AUG-1992

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OM nucleic - nucleic search, using sw model

Run on: January 23, 2005, 00:49:49 ; Search time 611 Seconds
(without alignments)
13936.836 Million cell updates/sec

Title: US-09-837-344-41

Sequence: 1 CAAGAACACCAAGCATCT.....AATATTATTGAACTATA 1482

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
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10: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1482	100.0	1482	9	US-09-837-344-41
2	1482	100.0	1482	10	US-09-837-344-41
3	1480.4	99.9	1482	9	US-09-837-344-45
4	1480.4	99.9	1482	10	US-09-837-344-45
5	1446	97.6	1493	9	US-09-837-344-38
6	1446	97.6	1493	10	US-09-837-344-38
7	950	64.1	950	9	US-09-837-344-32
8	950	64.1	950	10	US-09-837-344-32
9	472.8	31.9	988	9	US-09-837-344-34
10	472.8	31.9	988	10	US-09-837-344-34
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13	233.4	15.7	1300	17	US-10-668-749A-1	Sequence 1, Appli
14	153.2	10.3	1297	18	US-10-425-115-67697	Sequence 67697, A
15	151.2	10.2	6292	16	US-10-221-714A-461	Sequence 461, App
16	149.2	10.1	6767	16	US-10-221-714A-330	Sequence 330, App
17	145.8	9.8	1243	18	US-10-425-115-172717	Sequence 172717, A
18	145	9.6	1204	17	US-10-437-963-77858	Sequence 77858, A
19	142.4	9.6	1081	18	US-10-425-115-16756	Sequence 16756, A
20	139.4	9.4	9539	14	US-10-239-676-52	Sequence 52, Appli
21	139.4	9.4	9539	15	US-10-240-453-54	Sequence 54, Appli
22	137.8	9.3	6668	15	US-10-363-345A-1670	Sequence 1670, Ap
23	132.8	9.0	778	18	US-10-363-345A-2179	Sequence 2179, Ap
24	132.8	9.0	778	18	US-10-363-345A-2180	Sequence 2180, Ap
25	131.4	8.9	7442	16	US-10-221-714A-409	Sequence 409, App
26	129.8	8.8	521	18	US-10-425-115-38710	Sequence 38710, A
27	129.8	8.8	1762	18	US-10-363-345A-7529	Sequence 7529, Ap
28	129.8	8.8	1762	18	US-10-363-345A-7530	Sequence 7530, Ap
29	129.2	8.7	1595	18	US-10-363-345A-7533	Sequence 7533, Ap
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31	129	8.7	1200	18	US-10-363-345A-25801	Sequence 25801, A
32	129	8.7	1200	18	US-10-363-345A-25802	Sequence 25802, A
33	129	8.7	7597	15	US-10-311-455-1931	Sequence 986, App
34	129	8.7	14006	15	US-10-311-455-1931	Sequence 1931, App
35	128.6	8.7	3673778	15	US-10-312-841-1	Sequence 1, Appli
36	128.6	8.7	3673778	15	US-10-312-841-2	Sequence 2, Appli
37	127.4	8.6	3683	18	US-10-473-126-339	Sequence 339, App
38	127	8.6	1130	18	US-10-425-115-132399	Sequence 132399, A
39	127	8.6	3683	18	US-10-473-126-193	Sequence 193, App
40	126.2	8.5	880	18	US-10-425-115-53133	Sequence 53133, A
41	124.6	8.4	986	18	US-10-425-115-174478	Sequence 174478, A
42	123.8	8.4	1062	18	US-10-425-115-120013	Sequence 120013, A
43	123.4	8.3	3037	18	US-10-363-345A-40657	Sequence 40657, A
44	123.4	8.3	3037	18	US-10-363-345A-40658	Sequence 40658, A
45	123	8.3	12237	15	US-10-311-455-2331	Sequence 2331, Ap

ALIGNMENTS

RESULT 1
US-09-837-344-41
Sequence 41, Application US/09837344
Patent No. US2002004182A1
GENERAL INFORMATION:
APPLICANT: GUERIN-MARCHAND, Claudine
TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE
HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE
OF STIMULATING THE T LYMPHOCYTES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/837,344
FILING DATE: 19-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,625
FILING DATE: <Unknown>
APPLICATION NUMBER: FR 91 01286
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 22, 2005, 23:02:29 ; Search time 3390 Seconds

(without alignment)
15930.290 Million cell updates/sec

Title: US-09-837-344-41
Sequence: 1482
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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9: gb_esc9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	237.8	16.0	1434	9	AJ592058 Arabidops
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8	235	15.9	1654	9	CU118709 ISB1-7211
9	234.2	15.8	1797	9	CU066150 CH216-108
10	234	15.8	1829	9	CU109409 ISB1-51H2
11	233.8	15.8	1736	9	CU066373 CH216-108
12	233.6	15.8	1407	9	AJ592026 Arabidops
13	232.8	15.7	1512	9	CU113943 ISB1-59E2
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15	232.6	15.7	1811	9	CG753732 P048-4-G0
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17	231.4	15.6	1650	9	CU041163 CH216-51P
18	231.2	15.6	1762	9	CU082587 CH216-168
19	230.4	15.5	1824	9	CU081234 CH216-161
20	230.2	15.5	1727	9	CU118815 ISB1-7205
21	230	15.5	1632	9	CU082569 CH216-167
22	229.8	15.5	1616	9	CU081995 CH216-165
23	229.6	15.5	1630	9	CU078686 CH216-152
24	229.2	15.5	1457	9	CU082658 CH216-169

C	25	228.8	15.4	1566	9	CG757757 P053-1-D0
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C	31	228	15.4	2103	9	CU041093 CH216-51M
C	32	227.6	15.4	1712	9	CU078539 CH216-151
C	33	226.8	15.3	1547	9	CU066420 CH216-108
C	34	226.6	15.3	1377	9	CU077307 CH216-144
C	35	226.4	15.3	1716	8	CC222065 CH216-11A
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C	38	225.4	15.2	1482	9	AG332292 Mus muscu
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ALIGNMENTS

RESULT 1
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DEFINITION 0224m3 gmbpH3.1, G. Roman Reddy Plasmodium falciparum genomic
T09652 clone 0224m, genomic survey sequence.
ACCESSION T09652 GI:319484
VERSION T09652.1
KEYWORDS GSS.
SOURCE Plasmodium falciparum (malaria parasite P. falciparum)
ORGANISM Plasmodium falciparum
REFERENCE Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
AUTHORS 1 (bases 1 to 317)
Reddy, G.R., Chakrabarti, D., Schuster, S.M., Ferl, R.J., Almira, E.C.
and Dame, J.B.
Gene sequence tags from Plasmodium falciparum genomic DNA fragments
prepared by the genease activity of mung bean nuclease
Proc. Natl. Acad. Sci. U.S.A. 90, 9867-9871 (1993)
MEDLINE 94052193
PUBMED 8234327
Other GSSs: 0224m7

COMMENT

Contact: Dame JB
Dept. of Pathobiology, College of Veterinary Medicine
University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA
Tel: 352 352 4700
Fax: 352 392 9704
Email: damej@mail.vetmed.ufl.edu
Seg primer: T3
Class: shotgun.

FEATURES

source
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/mol_type="genomic DNA"
/db_xref="taxon:5833"
/clone="0224m"
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H3 isolate cultured in vitro, was digested at 500C
nuclease in the presence of 30x formamide at 500C
(Vernick, K.D., Imerski, R.B., and McCutchan, T.F. 1988.
Nucleic Acids Research 16:6883-6896). The ends of the
fragments were ligated using T4 DNA polymerase, and the
dephosphorylated pBluescript SK(+). Recombinant plasmids
transformed E. coli XL1-Blue."

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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 14, 2005, 20:21:26 ; Search time 211.5 Seconds
(without alignments)
5027.299 Million cell updates/sec

Title: US-09-837-344-41

Perfect score: 2486
Sequence: 1 CAGGACCAACCAAGCATCT.....AATATTATGAACTATATA 1482

Scoring table:

BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 4004546

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1561	62.8	316	2	AAR26941
5	969.5	33.0	462	2	AAR05766
6	770.5	31.0	318	2	AAR26943
7	603	24.3	117	4	AAR26937
8	376.5	14.3	419	4	ABG17301
9	376	15.1	1898	7	AAV30795
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11	361.5	14.5	412	2	AAW03626
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14	359	14.4	1162	3	AAV62331
15	359	14.4	1162	5	ABE05621
16	359	14.4	1162	5	ADJ65096
17	339.5	13.7	207	3	AB444672
18	339.5	13.5	562	2	AAR70491
19	332.5	13.4	1192	3	AAI18165
20	331	13.3	2274	3	ABE58657
21	330.5	13.3	2990	8	ADP29884
22	327.5	13.2	360	2	AAW03627
23	323.5	13.0	611	2	AAZ29039
24	323.5	13.0	611	4	AAU25510
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27	320	12.9	658	4	ABE5632
28	320	12.9	800	4	ABE71459
29	320	12.9	3616	8	ADP45530
30	319	12.8	1972	2	AAW00024
31	318	12.8	554	4	ABE59454
32	317.5	12.8	1937	8	ADQ17289
33	317.5	12.8	1937	8	ADQ17242
34	316	12.7	1180	7	ADP6151
35	315.5	12.7	1170	5	ABE05710
36	315.5	12.7	1170	7	ADP6789
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ALIGNMENTS

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DT	08-FEB-1993	(first entry)
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KW	Malaria; hepatocyte; sporozoite; T-cell epitope; B-cell epitope;	
KW	paludism; liver stage-specific antigen.	
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OS	Plasmodium falciparum.	
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PF	05-FEB-1992;	92WO-FR000104.
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PR	05-FEB-1991;	91FR-00001286.
XX		
XX	(INSP) INST PASTEUR.	
PA		
XX		
XX		
PI	Guerinmarchand C, Drulhe P;	
XX		

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OM nucleic - protein search, using frame_plus_nzp model

Run on: January 14, 2005, 20:38:17 ; Search time 44 Seconds
(without alignments)
4467,422 Million cell updates/sec

Title: US-09-837-344-41
Perfect score: 2486
Sequence: 1 CAGAGACACAAAGCATCT.....AATATTTTATGAACATAA 1482

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 478139 seqs, 6631800 residues
Total number of hits satisfying chosen parameters: 956278

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	554	22.3	107	3	US-08-098-327E-19
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11	359	14.4	1162	2	US-09-298-568-2
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14	336	13.5	608	4	US-09-270-767-32937	Sequence 32937, A
15	336	13.5	608	4	US-09-270-767-48154	Sequence 48154, A
16	323.5	13.0	611	4	US-09-216-393B-81	Sequence 81, Appl1
17	319	12.8	1972	4	US-08-875-435B-3	Sequence 3, Appl1
18	317.5	12.8	1937	4	US-09-538-092-918	Sequence 918, App
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21	314	12.6	1976	4	US-09-538-092-1078	Sequence 1078, Ap
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23	305	12.3	1939	4	US-09-538-092-915	Sequence 915, App
24	303.5	12.2	924	4	US-09-248-796A-18798	Sequence 18798, A
25	303	12.2	1939	3	US-09-310-187A-1	Sequence 1, Appl1
26	303	12.2	1939	4	US-09-538-092-917	Sequence 917, App
27	301	12.1	1857	4	US-09-917-254-91	Sequence 91, Appl
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31	299	12.0	3878	4	US-09-914-252-11	Sequence 11, Appl
32	298	12.0	735	4	US-10-164-595-80	Sequence 80, Appl
33	298	12.0	784	4	US-10-164-595-79	Sequence 79, Appl
34	298	12.0	843	4	US-10-164-595-54	Sequence 54, Appl
35	295	11.9	779	4	US-10-164-595-56	Sequence 56, Appl
36	294	11.8	683	6	5210183-3	Patent No. 5210183
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38	291	11.7	1239	4	US-09-291-417D-13	Sequence 13, Appl
39	282.5	11.4	885	2	US-08-533-306A-4	Sequence 4, Appl1
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ALIGNMENTS

RESULT 1
US-08-098-327E-31
; Sequence 31, Application US/08098327E
; Patent No. 6270771
; GENERAL INFORMATION:
; APPLICANT: GIBRIN-MARCHAND, Claudine
; APPLICANT: DRUIHE, Pierre
; TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE
; TITLE OF INVENTION: HEPATIC STAGES OF P. FALCIPARUM BEARING EPTOPES CAPABLE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/098,327E
; FILING DATE: 24-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 01286
; FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 010830-045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_nzp model

Run on: January 14, 2005, 21:00:12 ; Search time 211.5 Seconds

(without alignments)
5063.176 Million cell updates/sec

Title: US-09-837-344-41

Perfect score: 2486
Sequence: 1 CAAGACACAAAGCGACTCT.....AATATTATGAACTATATA 1482

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 3216122

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-Q=/cgnt2_1/uspro.spool.p/us09837344/runat_14012005_143844_4457/app.query.fasta_1.1671
-DB=Published Applications AA -QPM=fastan , SUPP=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62
-TRANS=human40.cdt -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09837344_CGN_1_1_233@runat_14012005_143844_4457
-NCPU=6 -ICPU=3 -NO MAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOF=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications AA:*

1:	/cgnt2_6/ptodata/1/pubpaa/us07_PUBCOMB.pep:*
2:	/cgnt2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3:	/cgnt2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4:	/cgnt2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5:	/cgnt2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6:	/cgnt2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7:	/cgnt2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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9:	/cgnt2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10:	/cgnt2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11:	/cgnt2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12:	/cgnt2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13:	/cgnt2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14:	/cgnt2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15:	/cgnt2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16:	/cgnt2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17:	/cgnt2_6/ptodata/1/pubpaa/US10D_NEW_PUB.pep:*
18:	/cgnt2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19:	/cgnt2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20:	/cgnt2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

No.	Score	Match	Length	DB	ID	Description
1	1549	62.3	316	9	US-09-837-344-31	Sequence 31, Appl
2	1549	62.3	316	10	US-09-900-963-31	Sequence 31, Appl
3	603	24.3	117	9	US-09-837-344-20	Sequence 20, Appl
4	603	24.3	117	10	US-09-900-963-20	Sequence 20, Appl
5	554	22.3	107	9	US-09-837-344-19	Sequence 19, Appl
6	554	22.3	107	10	US-09-900-963-19	Sequence 19, Appl
7	359	14.4	116	13	US-10-101-487-58	Sequence 58, Appl
8	359	14.4	116	11	US-09-894-273-2	Sequence 2, Appl
9	359	14.4	116	14	US-10-294-804-2	Sequence 2, Appl
10	359	14.4	116	17	US-10-194-804-2	Sequence 2, Appl
11	323.5	13.0	611	9	US-09-216-393-81	Sequence 81, Appl
12	323.5	13.0	611	14	US-10-321-856-81	Sequence 81, Appl
13	318.5	12.8	1961	14	US-10-028-248A-103	Sequence 103, Appl
14	318.5	12.8	1961	15	US-10-107-782-103	Sequence 103, Appl
15	317.5	12.8	1937	17	US-10-723-860-58	Sequence 58, Appl
16	317.5	12.8	1937	17	US-10-723-860-106	Sequence 106, Appl
17	315.5	12.7	1170	14	US-10-341-434-95	Sequence 95, Appl
18	315.5	12.7	1170	14	US-10-341-434-95	Sequence 95, Appl
19	315.5	12.7	1564	14	US-10-144-198-2	Sequence 2, Appl
20	315	12.7	1564	14	US-10-144-198-4	Sequence 4, Appl
21	315	12.7	1960	14	US-10-236-031B-62	Sequence 62, Appl
22	315	12.7	1960	15	US-10-028-248A-104	Sequence 104, Appl
23	313.5	12.6	1959	14	US-10-028-248A-106	Sequence 106, Appl
24	313.5	12.6	1959	15	US-10-107-782-36	Sequence 36, Appl
25	312.5	12.6	1959	14	US-10-028-248A-106	Sequence 106, Appl
26	312.5	12.6	1959	15	US-10-107-782-106	Sequence 106, Appl
27	311	12.5	240	13	US-10-101-487-75	Sequence 75, Appl
28	310.5	12.5	665	10	US-09-820-843A-107	Sequence 107, Appl
29	310	12.5	1963	14	US-10-369-493-5307	Sequence 5307, Appl
30	310	12.5	1963	14	US-10-369-493-5308	Sequence 5308, Appl
31	309.5	12.4	1956	14	US-10-369-493-6729	Sequence 6729, Appl
32	306.5	12.3	1790	14	US-10-369-493-1586	Sequence 1586, Appl
33	306	12.3	1959	14	US-10-028-248A-107	Sequence 107, Appl
34	306	12.3	1959	15	US-10-107-782-107	Sequence 107, Appl
35	305	12.3	621	15	US-10-108-260A-4409	Sequence 4409, Appl
36	305	12.3	1959	16	US-10-408-765A-2188	Sequence 2188, Appl
37	302.5	12.2	1130	14	US-10-369-493-6751	Sequence 6751, Appl
38	302.5	12.2	1959	17	US-10-798-037-4	Sequence 4, Appl
39	302	12.1	1958	16	US-10-408-765A-1629	Sequence 1629, Appl
40	301.5	12.1	1137	15	US-10-336-472-16	Sequence 16, Appl
41	301	12.1	1958	14	US-10-171-311-164	Sequence 164, Appl
42	301	12.1	1945	10	US-09-927-597-2	Sequence 2, Appl
43	301	12.1	1972	14	US-10-171-311-162	Sequence 162, Appl
44	301	12.1	1972	14	US-10-341-434-103	Sequence 103, Appl
45	301	12.1	1979	10	US-09-927-597-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-837-344-31
; Sequence 31, Application US/09837344
; Patent No. US20020041882A1

GENERAL INFORMATION:
APPLICANT: GUERIN-MARCHAND, Claudine

DRULHE, Pierre
TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE
HEPATITIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE
OF STIMULATING THE T LYMPHOCYTES

NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESSES:
ADDRESS: Burna, Doane, Swecker & Mathis
STREET: P.O. Box 1404

CITY: Alexandria
STATE: Virginia
COUNTRY: United States

ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: January 14, 2005, 20:37:21 ; Search time 59.5 Seconds
(without alignments)
4793.050 Million cell updates/sec

Title: US-09-837-344-41

Perfect score: 2486
Sequence: 1 CAAGAACACAAACGATCT.....AATATTATGAAACTATTA 1482

Scoring table:

BLOSUM62	Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5	
Fgapop 6.0	Fgapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xip
-O=/cgn2 1/USPTO.spool.p/US09837344/runat.14012005.143842.4425/app.query.fasta_1.1671
-DB=PIR 79 -OPMT=fastan -SUFFIX=rxr -MINMATCH=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFM=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US09837344 @CGN 1 1 80 @runat.14012005.143842.4425 -NCPU=6 -ICPU=3
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-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2406.5	96.8	1909	2 A45592	liver stage antigen
2	380.5	15.3	1407	1 S28589	trichohyalin - rab
3	380.5	15.3	1549	1 A40691	trichohyalin - she
4	376	15.1	1898	1 A45973	trichohyalin - hum
5	356	14.3	1017	2 T15598	hypothetical prote
6	353.5	14.2	737	2 T15597	hypothetical prote
7	332.5	13.4	1192	2 A71623	probable secreted
8	326.5	13.1	1979	1 S03166	myosin heavy chain
9	323.5	13.0	1039	2 S18189	myosin heavy chain
10	321	12.9	771	1 A33430	myosin heavy chain
11	319	12.8	1938	2 JC5421	h-caldesmon - chic
12	319	12.8	1972	2 JC5420	smooth muscle myos
13	318.5	12.8	1961	1 A61231	smooth muscle myos
14	317.5	12.8	1166	2 H86341	myosin heavy chain
					hypothetical prote

15	317.5	12.8	1937	2 I38055	myosin heavy chain
16	317.5	12.8	1992	2 A47297	myosin heavy chain
17	317.5	12.8	1432	2 B85431	trichohyalin like
18	316	12.7	1940	2 A29320	myosin heavy chain
19	314	12.6	1938	2 A59293	skeletal myosin he
20	314	12.6	1976	2 A59252	myosin heavy chain
21	313.5	12.6	1738	2 T14867	interaprin - blime
22	312.5	12.6	1959	1 A33977	myosin heavy chain
23	312	12.6	2007	1 B43402	myosin heavy chain
24	311.5	12.5	2139	2 T18296	myosin heavy chain
25	310.5	12.5	665	2 B71609	hypothetical prote
26	310.5	12.5	678	2 A54514	glutamic acid-rich
27	310	12.5	1963	1 MWK	myosin heavy chain
28	310	12.5	2116	2 A26655	myosin heavy chain
29	309.5	12.4	1956	2 T16416	hypothetical prote
30	309	12.4	1931	2 A59234	slow myosin heavy
31	309	12.4	1972	1 A41604	myosin heavy chain
32	307.5	12.4	1701	2 T09127	probable erythrocy
33	307	12.3	746	2 T47237	myosin II heavy ch
34	306.5	12.3	522	2 C96608	hypothetical prote
35	306.5	12.3	1790	2 S67593	transport protein
36	306	12.3	1999	1 S21801	myosin heavy chain
37	305.5	12.3	2017	1 A36014	myosin II heavy ch
38	305.5	12.3	2057	2 S61477	myosin II heavy ch
39	305	12.3	1964	2 A59282	nonmuscle myosin I
40	304.5	12.2	1959	1 A46762	myosin alpha heavy
41	304	12.2	451	2 G70241	hypothetical prote
42	303.5	12.2	1938	2 I49464	alpha cardiac myos
43	303.5	12.2	1939	2 I48175	myosin heavy chain
44	303	12.2	1526	2 A45605	mature-parasite-in
45	302.5	12.2	1130	2 T34081	hypothetical prote

ALIGNMENTS

RESULT 1
A45592
liver stage antigen LSA-1 - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 22-Nov-1993 #sequence revision 02-Dec-1994 #text change 09-Jul-2004
C:Accession: S24597; A45592; S29393; S34842; B45592; C45592; D45592
R:Zhu, J., Hollingdale, M.
Submitted to the EMBL Data Library, November 1990
A:Reference number: S24597
A:Accession: S24597
A:Molecule type: DNA
A:Residues: 1-1909 <ZHU>
A:Cross-references: UNIPROT:Q25893; EMBL:X56203; NID:99915; PID:99916
R:Zhu, J., Hollingdale, M.R., 223-226, 1991
Mol. Biochem. Parasitol., 48, 223-226, 1991
A:Title: Structure of Plasmodium falciparum liver stage antigen-1.
A:Reference number: A45592; MUID:92107224; PMID:1840628
A:Accession: A45592
A:Molecule type: DNA
A:Residues: 1-195;638-688;1165-1215;1590-1909 <ZH2>
A:Note: Sequence extracted from NCBI backbone (NCBIN:75010, NCBIN:75012, NCBIN:75014, R:Guerin-Marchand, C.; Drulhe, P.; Galey, B.; Londono, A.; Patapoutikou, J.; Beaudou Nature 329, 164-167, 1987
A:Title: A liver-stage-specific antigen of Plasmodium falciparum characterized by gen
A:Reference number: S29393; MUID:87315391; PMID:3306406
A:Accession: S29393
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 333-387 <GUB1>
A:Cross-references: EMBL:M28266
R:Guerin-Marchand, C.; Drulhe, P.; Galey, B.; Londono, A.; Patapoutikou, J.; Beaudou submitted to the EMBL Data Library, April 1992
A:Description: a liver-stage-specific antigen of plasmodium falciparum characterized
A:Reference number: S34842
A:Accession: S34842
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 323-381, 'HKAI' <GUB2>

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 14, 2005, 20:22:46 ; Search time 306 Seconds

(without alignments)
5573.237 Million cell updates/sec

Title: US-09-837-344-41

Sequence: 1 CAAAGAACACCAAGCATCT.....AATATTTTATGAACTATAA 1482

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 3650362

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ n2p.model -DEV=xlp
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-DB=UniProt_02 -Qfmt=fasta -SUPFIX=rup -TIMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-INITs-bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09837344@cgn2.1.1.307@runat.14012005.143842.4417 -NCPUS=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG.SCORES=0 -WAIT -OSPBLOCK=100 -LONGLOC
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: UniProt_02.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2478	99.7	493	2	Q25886
2	2406.5	96.8	1909	2	Q25893
3	2375.5	95.6	1596	2	Q81744
4	1451	58.4	280	2	Q25844
5	1450	58.3	280	2	Q25843
6	1447	58.2	280	2	Q25847
7	1447	58.2	280	2	Q25848
8	1447	58.2	280	2	Q25852
9	1445	58.1	280	2	Q25849
10	1445	58.0	280	2	Q25851
11	1443	58.0	280	2	Q25850
12	1442	57.8	280	2	Q25846
13	1437	57.7	280	2	Q25853
14	1434	57.6	280	2	Q25854
15	1433	57.6	280	2	Q25845
16	1432	57.6	280	2	Q25900

17	1430	57.5	280	2	Q25855	Q25855	plasmodium
18	1430	57.5	280	2	Q25858	Q25858	plasmodium
19	1428	57.4	280	2	Q27243	Q27243	plasmodium
20	1426	57.4	280	2	Q25889	Q25889	plasmodium
21	1366	54.9	264	2	Q9GTX5	Q9GTX5	plasmodium
22	770.5	31.0	318	2	Q25887	Q25887	plasmodium
23	468.5	18.8	978	2	Q7BAK4	Q7BAK4	plasmodium
24	429.5	17.3	3427	2	Q6IA79	Q6IA79	plasmodium
25	429.5	17.3	3427	2	AA038039	AA038039	plasmodium
26	398.5	16.0	1108	2	Q75JPS	Q75JPS	plasmodium
27	393.5	15.8	1508	2	Q75JPS	Q75JPS	plasmodium
28	393.5	15.8	1508	2	AA545390	AA545390	plasmodium
29	391.5	15.7	2349	2	Q81455	Q81455	plasmodium
30	391	15.7	1750	2	Q8X0H2	Q8X0H2	plasmodium
31	389	15.6	826	2	Q9VPS3	Q9VPS3	plasmodium
32	381.5	15.3	1003	2	Q91LX9	Q91LX9	plasmodium
33	381.5	15.3	1129	2	Q9GR71	Q9GR71	plasmodium
34	380.5	15.3	1407	1	TRHY_RABIT	TRHY_RABIT	plasmodium
35	380.5	15.3	1549	1	TRHY_SHEEP	TRHY_SHEEP	plasmodium
36	377.5	15.2	1089	2	Q40947	Q40947	plasmodium
37	377	15.2	1036	2	Q9DUM3	Q9DUM3	plasmodium
38	376	15.1	1898	1	TRHY_HUMAN	TRHY_HUMAN	plasmodium
39	370.5	14.9	10578	2	Q8ISF5	Q8ISF5	plasmodium
40	370.5	14.9	18519	2	Q8ISFP6	Q8ISFP6	plasmodium
41	370.5	14.9	18534	2	Q8ISF7	Q8ISF7	plasmodium
42	367.5	14.8	1192	2	Q869E1	Q869E1	plasmodium
43	366	14.7	791	2	Q9DGL1	Q9DGL1	plasmodium
44	366	14.7	2760	2	Q815Y2	Q815Y2	plasmodium
45	365	14.7	2275	2	Q81HVE	Q81HVE	plasmodium

ALIGNMENTS

RESULT 1
Q25886 PRELIMINARY: PRT: 493 AA.
AC Q25886;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Liver stage antigen-1 (Fragment).
OS Name=LSA-1;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94267224; PubMed=7515922;
RA Fidock D.A., Gras-Masse H., Lepers J., Brahimi K., Benmohamed L.,
RA Mellouk S., Guerin-Marchand C., Londono A., Raharimalala L.,
RA Meis J.F., Langsley G., Roussillon C., Tatar A., Druille P.,
RT "Plasmodium falciparum liver stage antigen-1 is well conserved and
RT contains potent B and T cell determinants".
RL J. Immunol. 153:190-204(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Fidock D.A., Gras-Masse H., Lepers J., Brahimi K., Benmohamed L.,
RA Mellouk S., Guerin-Marchand C., Londono A., Raharimalala L.,
RA Meis J.F., Langsley G., Roussillon C., Tatar A., Druille P.,
RT "The Plasmodium falciparum liver stage antigen LSA-1 is well conserved
RT and harbors major B- and T-cell epitopes".
RL J. Immunol. 0:0-0(1994).
DR EMBL; Z30320; CAA82975.1; -.
FT NON_TER
SQ SEQUENCE 493 AA; 59062 MW; FE252CC4FF469965 CRC64;

Alignment Scores:
Pred. No.: 6.85e-107
Score: 2478.00 Length: 493
Percent Similarity: 100.00% Matches: 493
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.68% Indels: 0
Gaps: 0